

SEQUENCE LISTING

<110> Novozymes A/S

<120> Trypsin like protease

<130> 10178

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<170> PatentIn version 3.2

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<212> DNA

<213> Fusarium solani

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<222> (52)..(804)

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<221> mat_peptide

<222> (127)..(804)

<223> 52-102: signal peptide and 53-126: pro-peptide

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Lys Phe Ala Ala Ile Leu Ala Leu Val Ala Pro Leu Val Ala Ala Arg		
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cct cag gac tca tca ccc atg atc gtt ggt gga act gct gcc agc gct	153	
Pro Gln Asp Ser Ser Pro Met Ile Val Gly Gly Thr Ala Ala Ser Ala		
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		5

ggt gac ttc ccc ttc atc gtc agc atc gcc tac aat ggt ggc cct tgg	201		
Gly Asp Phe Pro Phe Ile Val Ser Ile Ala Tyr Asn Gly Gly Pro Trp			
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tgc gga ggt acc ctc ctc aac gcc aac acc gtc atg act gct gcc cac	249	
Cys Gly Gly Thr Leu Leu Asn Ala Asn Thr Val Met Thr Ala Ala His		
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tgc acc caa ggt cgc tct gct agc gcc ttc cag gtc cgc gcc gga agt	297	
Cys Thr Gln Gly Arg Ser Ala Ser Ala Phe Gln Val Arg Ala Gly Ser		
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ctg aac cgc aac tcg ggt ggt gtt acc tct tcc gtt tct tcc atc agg	345	
Leu Asn Arg Asn Ser Gly Gly Val Thr Ser Ser Val Ser Ser Ile Arg		
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atc cat cct agc ttc agt agc tcg acc ctg aac aac gat gtt tcc atc	393	
Ile His Pro Ser Phe Ser Ser Ser Thr Leu Asn Asn Asp Val Ser Ile		
75	80	85

ctg aag ctg tcc acc ccc atc tcg act agc tcc act att tct tat ggt	441
Leu Lys Leu Ser Thr Pro Ile Ser Thr Ser Ser Thr Ile Ser Tyr Gly	
90 95 100 105	
cgc ctg gct gcg tcg ggc tct gac cct gtt gcc ggc tct gat gcc aca	489
Arg Leu Ala Ala Ser Gly Ser Asp Pro Val Ala Gly Ser Asp Ala Thr	
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gtt gct ggc tgg ggt gtc act tct cag ggc tct tcc agc tct ccc gtg	537
Val Ala Gly Trp Gly Val Thr Ser Gln Gly Ser Ser Ser Pro Val	
125 130 135	
gct ttg agg aag gtt acc att ccc atc gtc tcc cgc acc act tgc cga	585
Ala Leu Arg Lys Val Thr Ile Pro Ile Val Ser Arg Thr Thr Cys Arg	
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tcc cag tat ggc act tct gcc atc acc acc aac atg ttc tgc gct ggt	633
Ser Gln Tyr Gly Thr Ser Ala Ile Thr Thr Asn Met Phe Cys Ala Gly	
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ctt gct gag ggt aag gac tct tgc cag ggc gac agc ggc ggt ccc	681
Leu Ala Glu Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro	
170 175 180 185	
att gtc gat acc tcc aac act gtc att ggc att gtt tct tgg ggt gag	729
Ile Val Asp Thr Ser Asn Thr Val Ile Gly Ile Val Ser Trp Gly Glu	
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ggt tgt gct cag ccc aac tta tct ggt gtc tat gcc cga gtt gga tct	777
Gly Cys Ala Gln Pro Asn Leu Ser Gly Val Tyr Ala Arg Val Gly Ser	
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ctc cgc act tac atc gac ggc cag ctg taaattgctc ggtcggttgg	824
Leu Arg Thr Tyr Ile Asp Gly Gln Leu	
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gatggagtag gaatgctgag agtgtttgg tgagagttt gttgatagtc aagatccaag	944
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Pro Trp Cys Gly Gly Thr Leu Leu Asn Ala Asn Thr Val Met Thr Ala
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Ala His Cys Thr Gln Gly Arg Ser Ala Ser Ala Phe Gln Val Arg Ala
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Gly Ser Leu Asn Arg Asn Ser Gly Gly Val Thr Ser Ser Val Ser Ser
60 65 70

Ile Arg Ile His Pro Ser Phe Ser Ser Ser Thr Leu Asn Asn Asp Val
75 80 85

Ser Ile Leu Lys Leu Ser Thr Pro Ile Ser Thr Ser Ser Thr Ile Ser
90 95 100

Tyr Gly Arg Leu Ala Ala Ser Gly Ser Asp Pro Val Ala Gly Ser Asp
105 110 115

Ala Thr Val Ala Gly Trp Gly Val Thr Ser Gln Gly Ser Ser Ser Ser
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Pro Val Ala Leu Arg Lys Val Thr Ile Pro Ile Val Ser Arg Thr Thr
140 145 150

Cys Arg Ser Gln Tyr Gly Thr Ser Ala Ile Thr Thr Asn Met Phe Cys
155 160 165

Ala Gly Leu Ala Glu Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly
170 175 180

Gly Pro Ile Val Asp Thr Ser Asn Thr Val Ile Gly Ile Val Ser Trp
185 190 195

Gly Glu Gly Cys Ala Gln Pro Asn Leu Ser Gly Val Tyr Ala Arg Val
200 205 210 215

Gly Ser Leu Arg Thr Tyr Ile Asp Gly Gln Leu
220 225